



003300-589.ST25

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SEQUENCE LISTING

<110> ULF, Lindahl
LI, Jin-Ping

<120> DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a Process for Its Production

<130> 003300-589

<140> US 09/403,269
<141> 1999-10-18

<150> SE 9701454-2
<151> 1997-04-18

<150> PCT/SE98/00703
<151> 1998-04-17

<160> 13

<170> PatentIn version 3.0

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<212> DNA
<213> Human

<400> 1
gctgattctt ttctgtc

17

<210> 2
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<220>
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<222> (5)..(5)
<223> Amino acid 5 is Xaa wherein Xaa = any amino acid.

<400> 2

Pro Asn Asp Trp Xaa Val Pro Lys Gly Cys Phe Met Ala
1 5 10

<210> 3
<211> 11
<212> PRT
<213> Human

<220>
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<222> (2)..(10)
<223> Amino acids 2 and 10 are Xaa wherein Xaa = any amino acid.

<400> 3

Pro Xaa Asp Trp Thr Val Pro Lys Gly Xaa Phe
1 5 10

<210> 4

<211> 8

<212> PRT

<213> Human

<220>

<221> PEPTIDE

<222> (4)..(4)

<223> Amino acid 4 is Xaa wherein Xaa = any amino acid.

<400> 4

Pro Asn Asp Xaa Thr Val Pro Lys
1 5

<210> 5

<211> 15

<212> PRT

<213> Human

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Amino acids 1, 2 and 11 are Xaa wherein Xaa = any amino acid.

<400> 5

Xaa Xaa Ile Ala Pro Glu Thr Ser Glu Gly Xaa Ser Leu Gln Leu
1 5 10 15

<210> 6

<211> 10

<212> PRT

<213> Human

<400> 6

Gly Gly Trp Pro Ile Met Val Thr Arg Lys
1 5 10

<210> 7

<211> 8

<212> PRT

<213> Human

<400> 7

Phe Leu Ser Glu Gln His Gly Val
1 5

<210> 8

<211> 36

<212> PRT
 <213> Human

<220>
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 <222> (30)..(30)
 <223> Amino acid 30 is Xaa wherein Xaa = any amino acid.

<400> 8

Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile Tyr Asp
 1 5 10 15

Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Xaa Trp Asp
 20 25 30

Tyr His Thr Thr
 35

<210> 9<211> 25<212> DNA<213> Human<220><221> misc_feature<222> (14)..(23)<223> Nucleotides 14, 20 and 23 are "n" wherein "n" = any nucleotide.

<400> 9

ccgaattcaa rgcnatgytn ccnyt 25

<210> 10
 <211> 26
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (14)..(17)
 <223> Nucleotides 14 and 17 are "n" wherein "n" = any nucleotide.

<400> 10

ccgaattcga yytnmgnca tttatg 26

<210> 11
 <211> 25
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> Nucleotide 11 is "n" wherein "n" = any nucleotide.

<400> 11

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<210> 12
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<212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (73)..(1404)

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aag	aat	cag	ctc	ttc	act	gta	cat	tat	gtc	tca	aat	acc	cag	cta	att	Lys	Asn	Gln	Leu	Phe	Thr	Val	His	Tyr	Val	Ser	Asn	Thr	Gln	Leu	Ile	543
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Gly Leu Ser Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys	
190 195 200 205	
aag gtg gtt agg ttg att gcg aaa ggg aag ggc ttc ctt gac aac att	735
Lys Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile	
210 215 220	
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Thr Ile Ser Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp	
225 230 235	
tgg ctg gtg agg aac cag gat gag aaa ggc ggc tgg ccg att atg gtg	831
Trp Leu Val Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val	
240 245 250	
acc cgt aag tta ggg gaa ggc ttc aag tct tta gag cca ggg tgg tac	879
Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr	
255 260 265	
tcc gcc atg gcc caa ggg caa gcc att tct aca tta gtc agg gcc tat	927
Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr	
270 275 280 285	
ctc tta aca aaa gac cat ata ttc ctc aat tca gct tta agg gca aca	975
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Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe	
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atg aat aaa cat gac tgg tat gaa gaa tat cca act aca cct agc tct	1071
Met Asn Lys His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser	
320 325 330	
ttt gtt tta aat ggc ttt atg tat tct tta att ggg ctg tat gac tta	1119
Phe Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu	
335 340 345	
aaa gaa act gca ggg gaa aaa ctc ggg aaa gaa gcg agg tcc ttg tat	1167
Lys Glu Thr Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr	
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Glu Arg Gly Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr	
370 375 380	
ggc tca gga acc atc tat gac ctc cgg cac ttc atg ctt ggc att gcc	1263
Gly Ser Gly Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala	
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ccc aac ctg gcc cgc tgg gac tat cac acc acc cac atc aat caa ctg	1311
Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu	
400 405 410	
cag ctg ctt agc acc att gat gag tcc cca atc ttc aaa gaa ttt gtc	1359

Gln Leu Leu Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val
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Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln		
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Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu Ser His Tyr		
35	40	45

Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr		
50	55	60

Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp Thr Val Pro			
65	70	75	80

Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Phe Thr Asn		
85	90	95

Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln		
100	105	110

Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Phe Leu		
115	120	125

Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln		
130	135	140

Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Lys			
145	150	155	160

Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr

165

170

175

Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser
180 185 190

Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys Lys Val Val
195 200 205

Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser
210 215 220

Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val
225 230 235 240

Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys
245 250 255

Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met
260 265 270

Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr
275 280 285

Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr Ala Pro Tyr
290 295 300

Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys
305 310 315 320

His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu
325 330 335

Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr
340 345 350

Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly
355 360 365

Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly
370 375 380

Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu
385 390 395 400

Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu
405 410 415

Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp
420 425 430

Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn
435 440